Applicants have now submitted a substitute Sequence Listing and a corresponding Computer-Readable Sequence Listing. Contents of the paper copy of the substitute Sequence Listing and the Computer-Readable Sequence Listing are identical. Support for all the sequences listed in the substitute Sequence Listing can be found in the present application. No new matter is introduced by the submission of the substitute Sequence Listing and the Computer-Readable Sequence Listing.

Applicants submit that this application is now in condition for examination on the merits. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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MARKED-UP COPY OF
PRELIMINARY AMENDMENT AND STATEMENT

IN THE SPECIFICATION

Please replace the paragraph beginning on page 4, line 25, through page 5, line 11, with the following paragraph:

--PCR (polymerase chain reaction) is performed by using chromosomal DNA of *Brevibacterium lactofermentum* such as *Brevibacterium lactofermentum* ATCC13869 as a template and primers having nucleotide sequences of regions in the *g1tBD* genes of *Escherichia Coli* K-12 (*Gene, vol. 60*, pp. 1-11 (1987) and yeast (*Saccharomyces cerevisiae*, GenBank Accession No. X89221) exhibiting high homology, for example, those having nucleotide sequences of SEQ ID NOS: 1 and 2 shown in Sequence Listing, to obtain a DNA fragment of about 1.4 kb. *Brevibacterium lactofermentum* ATCC13869 can be obtained from ATCC (the American Type Culture Collection: [12301 Parklawn Drive, Rockville, Maryland, 20852] 10801 University Boulevard, Manassas, VA 20110-2209, United States of America).--

Please replace the paragraph on page 9, line 24, through page 10, line 26, with the following paragraph:

--A DNA coding for substantially the same protein as a constituent of ABC transporter can be obtained by expressing DNA having such a mutation as described above in an appropriate cell, and examining characteristics of an expressed product. A DNA coding for substantially the same protein as a constituent of ABC transporter can also be obtained by

isolating a DNA hybridizable with a nucleotide sequence coding for each constituent or a probe prepared from such a nucleotide sequence, for example, the nucleotide sequence of nucleotide numbers 1117 to 1725 in SEQ ID NO: 7 or a probe prepared from this nucleotide sequence, for ATPase under a stringent condition, and coding for a protein having the characteristics of the constituent from a DNA coding for each protein having mutation or from a cell harboring it. The "stringent condition" referred to herein is a condition under which a so-called specific hybrid is formed, but a non-specific hybrid is not formed. It is difficult to clearly define this condition by using numerical values. However, for example, the stringent condition includes a condition under which two of DNAs having high homology, for example, two of DNAs having homology of not less than [40%] 60% are hybridized with each other, but two of DNAs having homology lower than the above level are not hybridized with each other. Alternatively, the stringent condition is exemplified by a hybridization condition represented by salt concentrations of 1 x SSC, 0.1% SDS, preferably 0.1 x SSC, 0.1% SDS, at 60°C, which is an ordinary condition of washing in Southern hybridization.--

IN THE CLAIMS

--4. (Amended) The DNA according to Claim 3, wherein the stringent condition is a condition in which [washing] hybridization is performed at 60°C and a salt concentration corresponding to 1 x SSC and 0.1% SDS.

8. (Amended) The DNA according to Claim 7, wherein the stringent condition is a condition in which [washing] hybridization is performed at 60°C and a salt concentration corresponding to 1 x SSC and 0.1% SDS.

12. (Amended) The DNA according to Claim 11, wherein the stringent condition is a condition in which [washing] hybridization is performed at 60°C and at a salt concentration corresponding to 1 x SSC and 0.1% SDS.--